

Abstract

The invention concerns a method for the identification of cytosine methylation patterns in genomic DNA samples, wherein

a) a genomic DNA sample is chemically treated such that cytosine and 5-methylcytosine react differently and a different base pairing behavior of the two products results in the duplex;

b) parts of the thus-treated DNA sample are enzymatically amplified;

c) the amplified parts of the thus-treated DNA sample bind to a surface;

d) a set of probes of different nucleobase sequences, each of which contains the dinucleotide sequence 5'-CpG-3' at least once, is hybridized to the immobilized DNA sample;

e) the non-hybridized probes are separated;

f) the hybridized probes are analyzed in a mass spectrometer, wherein the position of the probes on the sample holder permits a classification of the hybridizing DNA sample;

g) Assignment of the peak pattern obtained from the mass spectra to the methylation pattern and comparison of the new data with a database.